

XM048113	1	-----
ANH401	1	MAAVSLRLGDLVWGKLRGPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
AF326966	1	MAAVSLRLGDLVWGKLRGPPWPGKIVNPPKDLKKPRGKKCFFVKFFGTEDHAWIKVEQL
XM048113	1	-----
ANH401	61	KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSDDKNRRNSSEERSRP
AF326966	61	KPYHAHKEEMIKINKGKRFQQAVDAVEEFLRRAKGKDQTSSHNSDDKNRRNSSEERSRP
XM048113	1	-----
ANH401	121	NSGDEKRKLSLSEGKVKKNMGEKKRVSSEGSERGSKSPLKRAQEQSPRKRGRPPKDEKD
AF326966	121	NSGDEKRKLSLSEGKVKKNMGEKKRVSSEGSERGSKSPLKRAQEQSPRKRGRPPKDEKD
XM048113	1	-----
ANH401	181	LTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK
AF326966	181	LTIPESSTVKGMMAGPMAAFKWQPTASEPVKDADPHFHHFLLSQTEKPAVCYQAITKKLK
XM048113	1	-----
ANH401	241	ICEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSIVSNLLKMGHTVTVWNRTA
AF326966	241	ICEEETGSTSIQAADSTAVNGSITPTDKKIGFLGLGLMGSIVSNLLKMGHTVTVWNRTA
XM048113	24	EKCDLFQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPGSGLQGIRPGKCYVDM
ANH401	301	EKCDLFQEGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPGSGLQGIRPGKCYVDM
AF326966	301	EK-----EGARLGRTPAEVVSTCDITFACVSDPKAAKDLVLGPGSGLQGIRPGKCYVDM
XM048113	84	STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM
ANH401	361	STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM
AF326966	355	STVDADTVTELAQVIVSRGGRFLEAPVSGNQQLSNDGMLVILAAGDRGLYEDCSSCFQAM
XM048113	144	GKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASI
ANH401	421	GKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAHVTGQSQQTLLDILNQGQLASI
AF326966	415	GKTSFFLGEVGNAAKMMLIVNMVQGSFMATIAEGLTLAQVTGQSQQTLLDILNQGQLASI
XM048113	204	FLDQKCQNILQGNFKPDFYLYKIQKDLRLAIALGDAVNHPPTPMAAAANEVYKRAKALDQS
ANH401	481	FLDQKCQNILQGNFKPDFYLYKIQKDLRLAIALGDAVNHPPTPMAAAANEVYKRAKALDQS
AF326966	475	FLDQKCQNILQGNFKPDFYLYKIQKDLRLAIALGDAVNHPPTPMAAAANEVYKRAKALDQS
XM048113	264	DNDMSAVYRAYIH
ANH401	541	DNDMSAVYRAYIH
AF326966	535	DNDMSAVYRAYIH

Fig. 1